

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Blank, Gregory S.
Narindray, Daljit S.
Zapata, Gerardo A.
- (ii) TITLE OF INVENTION: Protein Recovery
- 10 (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
20 (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: to be assigned
(B) FILING DATE: 21-Jan-2004
30 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 09/940166
(B) FILING DATE: 27-Aug-2001
35
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 09/460587
(B) FILING DATE: 14 Dec-1999
- 40 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 09/097309
(B) FILING DATE: 12-Jun-1998
- (vii) PRIOR APPLICATION DATA:
45 (A) APPLICATION NUMBER: 60/050951
(B) FILING DATE: 13-JUN-1997
- (viii) ATTORNEY/AGENT INFORMATION:
50 (A) NAME: Lee K. Tan
(B) REGISTRATION NUMBER: 39447
(C) REFERENCE/DOCKET NUMBER: P1105R1D1C2
- (ix) TELECOMMUNICATION INFORMATION:
55 (A) TELEPHONE: 650/225-4462
(B) TELEFAX: 650/952-9881
- (2) INFORMATION FOR SEQ ID NO:1:
- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5	Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly	1	5	10	15
	Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Tyr Thr Phe Thr	20	25	30	
10	Glu Tyr Thr Met His Trp Met Arg Gln Ala Pro Gly Lys Gly Leu	35	40	45	
	Glu Trp Val Ala Gly Ile Asn Pro Lys Asn Gly Gly Thr Ser His	50	55	60	
15	Asn Gln Arg Phe Met Asp Arg Phe Thr Ile Ser Val Asp Lys Ser	65	70	75	
	Thr Ser Thr Ala Tyr Met Gln Met Asn Ser Leu Arg Ala Glu Asp	80	85	90	
20	Thr Ala Val Tyr Tyr Cys Ala Arg Trp Arg Gly Leu Asn Tyr Gly	95	100	105	
	Phe Asp Val Arg Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val	110	115	120	
25	Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu	125	130	135	
	Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly	140	145	150	
	Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp	155	160	165	
35	Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val	170	175	180	
	Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val	185	190	195	
	Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn	200	205	210	
45	His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys	215	220	225	
	Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu	230	235	240	
50	Leu	241			

(2) INFORMATION FOR SEQ ID NO:2:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 214 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	
	1				5					10					15	
5	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Asn	
					20					25					30	
	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	
					35					40					45	
10	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser	Thr	Leu	His	Ser	Gly	Val	Pro	Ser	
					50					55					60	
	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	
					65					70					75	
15	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	
					80					85					90	
	Gly	Asn	Thr	Leu	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	
20					95					100					105	
	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	
					110					115					120	
25	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	
					125					130					135	
	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	
					140					145					150	
30	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	
					155					160					165	
	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	
35					170					175					180	
	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	
					185					190					195	
40	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	
					200					205					210	
	Arg	Gly	Glu	Cys												
					214											

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

55	Leu	Gly	Gly	Arg	Met	Lys	Gln	Leu	Glu	Asp	Lys	Val	Glu	Glu	Leu	
	1				5					10					15	
	Leu	Ser	Lys	Asn	Tyr	His	Leu	Glu	Asn	Glu	Val	Ala	Arg	Leu	Lys	
					20					25					30	
60	Lys	Leu	Val	Gly	Glu	Arg										
					35	36										

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 7

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2143 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC 50
 TCATTGCTGA GTTGTATTAT AAGCTTTGGA GATTATCGTC ACTGCAATGC 100
 TTCGCAATAT GCGCAAAAT GACCAACAGC GGTGATTGA TCAGGTAGAG 150
 GGGGCGCTGT ACGAGGTAAA GCCCGATGCC AGCATTCCTG ACGACGATAC 200
 GGAGCTGCTG CCGGATTACG TAAAGAAGTT ATTGAAGCAT CCTCGTCAGT 250
 AAAAAGTTAA TCTTTTCAAC AGCTGTCATA AAGTTGTCAC GGCCGAGACT 300
 TATAGTCGCT TTGTTTTTAT TTTTAAATGT ATTTGTAAC AGAATTTCGAG 350
 CTCGCCGGGG ATCCTCTAGA GGTGAGGTG ATTTTATGAA AAAGAATATC 400
 GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA 450
 CGCTGATATC CAGATGACCC AGTCCCCGAG CTCCCTGTCC GCCTCTGTGG 500
 GCGATAGGGT CACCATCACC TGTCGTGCCA GTCAGGACAT CAACAATTAT 550
 CTGAAGTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA 600
 CTATACCTCC ACCCTCCACT CTGGAGTCCC TTCTCGCTTC TCTGGTTCTG 650
 GTTCTGGGAC GGATTACACT CTGACCATCA GCAGTCTGCA ACCGGAGGAC 700
 TTCGCAACTT ATTACTGTCA GCAAGGTAAT ACTCTGCCGC CGACGTTCCG 750
 ACAGGGCAGC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA CCATCTGTCT 800
 TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT 850
 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA 900
 GGTGGATAAC GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC 950
 AGGACAGCAA GGACAGCACC TACAGCCTCA GCAGCACCCCT GACGCTGAGC 1000

AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA 1050
 GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTAAAG 1100
 5 CTGATCCTCT ACGCCGGACG CATCGTGGCG CTAGTACGCA AGTTCACGTA 1150
 AAAACGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 1200
 10 TCTTCTTGCA TCTATGTTCTG TTTTCTCTAT TGCTACAAAC GCGTACGCTG 1250
 AGGTTTCAGCT GGTGGAGTCT GGCAGTGGCC TGGTGCAGCC AGGGGGCTCA 1300
 CTCCGTTTGT CCTGTGCAAC TTCTGGCTAC ACCTTTACCG AATACACTAT 1350
 15 GCACTGGATG CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGCAGGGA 1400
 TTAATCCTAA AAACGGTGGT ACCAGCCACA ACCAGAGGTT CATGGACCGT 1450
 TTCACTATAA GCGTAGATAA ATCCACCAGT ACAGCCTACA TGCAAATGAA 1500
 20 CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTATTGTGCT AGATGGCGAG 1550
 GCCTGAACTA CGGCTTTGAC GTCCGTTATT TTGACGTCTG GGGTCAAGGA 1600
 25 ACCCTGGTCA CCGTCTCCTC GGCCTCCACC AAGGGCCCAT CCGTCTTCCC 1650
 CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT 1700
 GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA 1750
 30 GCGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC 1800
 AGGACTCTAC TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG 1850
 35 GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCAG CAACACCAAG 1900
 GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAATC ACACATGCCC 1950
 GCCGTGCCCA GCACCAGAAC TGCTGGGCGG CCGCATGAAA CAGCTAGAGG 2000
 40 ACAAGGTCGA AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGTG 2050
 GCAAGACTCA AAAAGCTTGT CGGGGAGCGC TAAGCATGCG ACGGCCCTAG 2100
 45 AGTCCCTAAC GCTCGGTTGC CGCCGGGCGT TTTTATTGT TAA 2143

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 237 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

55 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 -23 -20 -15 -10
 Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser
 60 -5 1 5
 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
 10 15 20

	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Asn	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln
	25							30					35		
5	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser
	40							45					50		
	Thr	Leu	His	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser
	55							60					65		
10	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp
	70							75					80		
	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Pro	Thr
15	85							90					95		
	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala
	100							105					110		
20	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser
	115							120					125		
	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg
	130							135					140		
25	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly
	145							150					155		
	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr
30	160							165					170		
	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
	175							180					185		
35	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser
	190							195					200		
	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys			
	205							210				214			

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

50	Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe
	-23			-20				-15					-10		
	Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Val	Gln	Leu	Val	Glu	Ser
			-5					1					5		
55	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys
	10							15					20		
	Ala	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Glu	Tyr	Thr	Met	His	Trp	Met
60	25							30					35		
	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Gly	Ile	Asn
	40							45					50		

	Pro	Lys	Asn	Gly	Gly	Thr	Ser	His	Asn	Gln	Arg	Phe	Met	Asp	Arg	
			55					60					65			
5	Phe	Thr	Ile	Ser	Val	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Gln	
			70					75					80			
	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
			85					90					95			
10	Arg	Trp	Arg	Gly	Leu	Asn	Tyr	Gly	Phe	Asp	Val	Arg	Tyr	Phe	Asp	
			100					105					110			
	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	
15			115					120					125			
	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	
			130					135					140			
20	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	
			145					150					155			
	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	
			160					165					170			
25	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	
			175					180					185			
	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	
30			190					195					200			
	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	
			205					210					215			
35	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	
			220					225					230			
	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Arg	Met	Lys	
			235					240					245			
40	Gln	Leu	Glu	Asp	Lys	Val	Glu	Glu	Leu	Leu	Ser	Lys	Asn	Tyr	His	
			250					255					260			
	Leu	Glu	Asn	Glu	Val	Ala	Arg	Leu	Lys	Lys	Leu	Val	Gly	Glu	Arg	
45			265					270					275		277	